

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## APPLICANT:

5 NAME: The Procter & Gamble Company  
STREET: One Procter & Gamble Plaza  
CITY: Cincinnati, OHIO  
COUNTRY: USA  
POSTAL CODE: 45202

10 TITLE OF INVENTION: Detergent compositions comprising a mannanase and a  
soil release polymer.

NUMBER OF SEQUENCES: 6

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## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
20 SOFTWARE: PatentIn Release # 1.0 Version 1.25 (EPO)

## SEQ ID NO:1

## SEQUENCE CHARACTERISTICS:

25 LENGTH: 1407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

30 MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE

## FEATURE:

NAME/KEY: CDS  
35 LOCATION: 1-1482

005040" 05958460

## SEQUENCE DESCRIPTION: SEQ ID NO: 1

5 ATGAAAAAAAAAGTTATCACAGATTTATCATTTAATTATTTGCACACTTATAATA  
AGTGTGGGAATAATGGGGATTACAACGTCCCCATCAGCAGCAAGTACAGGC  
TTTTATGTTGATGGCAATACGTTATATGACGCAAATGGGCAGCCATTTGTCAT  
GAGAGGTATTAACCATGGACATGCTTGGTATAAAGACACCGCTTCAACAGCT  
ATTCCTGCCATTGCAGAGCAAGGCGCCAACACGATTCTGATTGTTTTATCAG  
10 ATGGCGGTCAATGGGAAAAAGACGACATTGACACCATTCGTGAAGTCATTG  
AGCTTGCGGAGCAAAATAAAATGGTGGCTGTCGTTGAAGTTCATGATGCCA  
CGGGTCGCGATTGCGCGAGTGATTTAAATCGAGCCGTTGATTATTGGATAG  
AAATGAAAGATGCGCTTATCGGTAAAGAAGATACGGTTATTATTAACATTGCA  
AACGAGTGGTATGGGAGTTGGGATGGCTCAGCTTGGGCCGATGGCTATATT  
15 GATGTCATTCCGAAGCTTCGCGATGCCGGCTTAACACACACCTTAATGGTTG  
ATGCAGCAGGATGGGGGCAATATCCGCAATCTATTCATGATTACGGACAAG  
GAGTATGCTGGTGGTATGCTAACACTGTTAGATCAAATATTGATAGAGTCA  
TAGATCAAGACCTTGCTCTCGTAATAGGTGAATTCGGTCATAGACATACTGA  
TGGTGATGTTGATGAAGATAACAATCCTTAGTTATTCTGAAGAACTGGCACA  
20 GGGTGGCTCGCTTGGTCTTGGAAGGCAACAGTACCGAATGGGACTATTTA  
GACCTTTCAGAAGACTGGGCTGGTCAACATTTAACTGATTGGGGGAATAGAA  
TTGTCCACGGGGCCGATGGCTTACAGGAAACCTCCAAACCATCCACCGTAT  
TGACTTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG  
25 GCCCTTGGTCCGTAACAGAATGGGGTGCTTCAGGTAACACTCTTTAAAAGC  
CGATGTAAATTTAACCTCAAATTCTTCACATGAACTGTATAGTGAACAAAGTC  
GTAATCTACACGGATACTCTCAGCTCAACGCAACCGTTCCGCATGCCAATTG  
GGGAAATCCCGGTAATGGCATGAATGCAAGACTTTACGTGAAAACGGGCTC  
TGATTATACATGGCATAGCGGTCTTTTACACGTATCAATAGCTCCAACCTCA  
30 GGAACAACGTTATCTTTTGATTAAACAACATCGAAAATAGTCATCATGTTAG  
GGAAATAGGCGTGCAATTTTCAGCGGCAGATAATAGCAGTGGTCAAACCTGC  
TCTATACGTTGATAACGTTACTTTAAGATAG

005040" 05454601

**SEQ ID NO:2****5 SEQUENCE CHARACTERISTICS:**

LENGTH: 493 amino acids

TYPE: amino acid

TOPOLOGY: linear

**10 MOLECULE TYPE: protein**

SEQUENCE DESCRIPTION: SEQ ID NO: 2

005040" 05958450

15 MKKKLSQIYHLIICTLIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN  
HGHAWYKDTASTAIPAIAEQGANTIRIVLSGGQWEKDDIDTIREVIELAEQNKM  
VAVVEVHDATGRDSRSDLNRAVDYWIEMKDALIGKEDTVIINIANEWYGSWDGS  
AWADGYIDVIPKL RDAGLTHTLMVDAAGWGQYPQSIHDY GQDVFNADPLKNTM  
FSIHMYEYAGGDANTVRSNIDRVIDQDLALVIGEF GHRHTDGDVDEDTILSYSEE  
TGTGWLAWSWKGNSTEW DYLDLSEDWAGQH L TDWGNRIVHGADGLQETSKP  
STVFTDDNGGHPEPPTATTLYDFEGSTQGWHG SNVTGGPWSVTEWGASGN Y  
20 SLKADVNLT SNSSHELYSEQSRNLHGYSQLNATVRHANWGNPGNGMNARLYV  
KTGSDYTWHSGPFTRINSSNSGTTLSFDLNNIENSHHVREIGVQFSAADNSSGQ  
TALYVDNVTLR

**25 SEQ ID NO:3****SEQUENCE CHARACTERISTICS:**

LENGTH: 1407 base pairs

TYPE: nucleic acid

**30 STRANDEDNESS: single**

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

**35 SEQUENCE DESCRIPTION: SEQ ID NO: 3**

ATGAAAAAAAAAGTTATCACAGATTTATCATTTAATTATTTGCACACTTATAATA  
AGTGTGGGAATAATGGGGATTACAACGTCCCCATCAGCAGCAAGTACAGGC  
TTTTATGTTGATGGCAATACGTTATATGACGCAAATGGGCAGCCATTTGTCAT  
GAGAGGTATTAACCATGGACATGCTTGGTATAAAGACACCGCTTCAACAGCT  
5 ATTCCTGCCATTGCAGAGCAAGGCGCCAACACGATTCGTATTGTTTTATCAG  
ATGGCGGTCAATGGGAAAAAGACGACATTGACACCATTTCGTGAAGTCATTG  
AGCTTGCGGAGCAAAATAAAATGGTGGCTGTCGTTGAAGTTCATGATGCCA  
CGGGTCGCGATTTCGCGCAGTGATTTAAATCGAGCCGTTGATTATTGGATAG  
AAATGAAAGATGCGCTTATCGGTAAAGAAGATACGGTTATTATTAACATTGCA  
10 AACGAGTGGTATGGGAGTTGGGATGGCTCAGCTTGGGCCGATGGCTATATT  
GATGTCATTCCGAAGCTTCGCGATGCCGGCTTAACACACACCTTAATGGTTG  
ATGCAGCAGGATGGGGGCAATATCCGCAATCTATTCATGATTACGGACAAG  
ATGTGTTTAATGCAGATCCGTAAAAAATACGATGTTCTCCATCCATATGTAT  
GAGTATGCTGGTGGTGAAGTACACTGTTAGATCAAATATTGATAGAGTCA  
15 TAGATCAAGACCTTGCTCTCGTAATAGGTGAATTCGGTCATAGACATACTGA  
TGGTGAATGTTGATGAAGATAACAATCCTTAGTTATTCTGAAGAACTGGCACA  
GGGTGGCTCGCTTGGTCTTGAAAGGCAACAGTACCGAATGGGACTATTTA  
GACCTTTCAGAAGACTGGGCTGGTCAACATTTAACTGATTGGGGGAATAGAA  
TTGTCCACGGGGCCGATGGCTTACAGGAAACCTCCAAACCATCCACCGTAT  
20 TTACAGATGATAACGGTGGTCACCCTGAACCGCCAACTGCTACTACCTTGTA  
TGACTTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG  
GCCCTTGGTCCGTAACAGAATGGGGTGGCTTCAGGTAACCTACTCTTTAAAGC  
CGATGTAAATTTAACCTCAAATTCTTCACATGAACTGTATAGTGAACAAAGTC  
GTAATCTACACGGATACTCTCAGCTCAACGCAACCGTTTCGCCATGCCAATTG  
25 GGGAAATCCCGGTAATGGCATGAATGCAAGACTTTACGTGAAAACGGGCTC  
TGATTATACATGGCATAGCGGTCCTTTTACACGTATCAATAGCTCCAACTCA  
GGAACAACGTTATCTTTTGATTTAAACAACATCGAAAATATCATCATGTTAGG  
GAAATAG

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**SEQ ID NO:4**

SEQUENCE CHARACTERISTICS:

LENGTH: 468 amino acids

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TYPE: amino acid

TOPOLOGY: linear

005070 05958460

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4

5 MKKKLSQIYHLIICTLIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN  
HGHAWYKDTASTAIPAIAEQGANTIRIVLSDGGQWEKDDIDTIREVIELAEQNKM  
VAVVEVHDATGRDSRSDLNRAVDYWIEMKDALIGKEDTVIINIANEWYGSWDGS  
AWADGYIDVIPKLRLDAGLTHLTMVDAAGWGQYPQSIHDYGQDVFNADPLKNTM  
FSIHMYEYAGGDANTVRSNIDRVIDQDLALVIGEFGRHTDGDVDEDTILSYSEE  
10 TGTGWLAWSWKGNSTEWLDYLDLSEDWAGQHLLTDWGNRIVHGADGLQETSKP  
STVFTDDNGGHPEPPTATTLYDFEGSTQGWHGNSVTGGPWSVTEWGASGNY  
SLKADVNLTSSSHELSEYSESRNLHGYSQLNATVRHANWGNPGNGMNRALYV  
KTGSDYTWHS GP FTRINSSNSGTTL SFDLNNIENIIMLGK

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**SEQ ID NO:5**

SEQUENCE CHARACTERISTICS:

LENGTH: 1029 base pairs

20 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

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SEQUENCE DESCRIPTION SEQ ID No:5

5' AAT TGG CGC ATA CTG TGT CGC CTG TGA ATC CTA ATG CCC AGC  
AGA CAA CAA AAA CAG TGA TGA ACT GGC TTG CGC ACC TGC CGA ACC  
30 GAA CGG AAA ACA GAG TCC TTT CCG GAG CGT TCG GAG GTT ACA GCC  
ATG ACA CAT TTT CTA TGG CTG AGG CTG ATA GAA TCC GAA GCG CCA  
CCG GGC AAT CGC CTG CTA TTT ATG GCT GCG ATT ATG CCA GAG GAT  
GGC TTG AAA CAG CAA ATA TTG AAG ATT CAA TAG ATG TAA GCT GCA  
ACG GCG ATT TAA TGT CGT ATT GGA AAA ATG GCG GAA TTC CGC AAA  
35 TCA GTT TGC ACC TGG CGA ACC CTG CTT TTC AGT CAG GGC ATT TTA  
AAA CAC CGA TTA CAA ATG ATC AGT ATA AAA ACA TAT TAG ATT CAG

CAA CAG CGG AAG GGA AGC GGC TAA ATG CCA TGC TCA GCA AAA TTG  
CTG ACG GAC TTC AAG AGT TGG AGA ACC AAG GTG TGC CTG TTC TGT  
TCA GGC CGC TGC ATG AAA TGA ACG GCG AAT GGT TTT GGT GGG GAC  
TCA CAT CAT ATA ACC AAA AGG ATA ATG AAA GAA TCT CTC TAT ATA  
5 AAC AGC TCT ACA AGA AAA TCT ATC ATT ATA TGA CCG ACA CAA GAG  
GAC TTG ATC ATT TGA TTT GGG TTT ACT CTC CCG ACG CCA ACC GAG  
ATT TTA AAA CTG ATT TTT ACC CGG GCG CGT CTT ACG TGG ATA TTG  
TCG GAT TAG ATG CGT ATT TTC AAG ATG CCT ACT CGA TCA ATG GAT  
ACG ATC AGC TAA CAG CGC TTA ATA AAC CAT TTG CTT TTA CAG AAG  
10 TCG GCC CGC AAA CAG CAA ACG GCA GCT TCG ATT ACA GCC TGT TCA  
TCA ATG CAA TAA AAC AAA AAT ATC CTA AAA CCA TTT ACT TTC TGG  
CAT GGA ATG ATG AAT GGA GCG CAG CAG TAA ACA AGG GTG CTT CAG  
CTT TAT ATC ATG ACA GCT GGA CAC TCA ACA AGG GAG AAA TAT GGA  
ATG GTG ATT CTT TAA CGC CAA TCG TTG AGT GAA TCC GGG ATC 3'

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**SEQ ID NO:6****SEQUENCE CHARACTERISTICS:**

20 LENGTH: 363 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 6

ydhT 1  
LFKKHTISLLIIFLLASAVLAKPIEAHTVSPVNPNAQQTTKTVMNWL AHL 50  
30 ydhT 51  
PNRTENRVLSGAFGGYSHDTFSMAEADRIRSATGQSPA IYGCDYARGWLE 100  
ydhT 101  
TANIEDSIDVSCNGDLMSYWKN GGIPQISLHLANPAFQSGHF KTPITNDQ 150  
ydhT 151  
35 YKNILDSATAEGKRLNAML SKIADGLQELENQGVPV LFRPLHEMNGE WFW 200

ydhT 201  
WGLTSYNQKDNERISLYKQLYKKIYHYMTDTRGLDHLIWWYSPDANRDFK 250  
ydhT 251  
TDFYPGASYVDIVGLDAYFQDAYSINGYDQLTALNKPFAFTEVGPQTANG 300  
5 ydhT 301  
SFDYSLFINAIKQKYPKTIYFLAWNDEWSAAVNKGASALYHDSWTLNKGE 350  
ydhT 351  
IWNGDSLTPIVE\*. 363

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